

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:40 ; Search time 2351.15 Seconds

(Without alignments) updates/sec
161.303 Million cell updates/sec

Title: US-09-851-670-14
Perfect score: 23
Sequence: 1 gagaacacccgcgtctcgcaaa 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 secs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

11: gb_sts:*

6: gb_pat:*

7: gb_ph:*

8: gb_p1:*

9: gb_pr:*

10: gb_lo:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Result No.	Score	Query Match Length	DB ID	Description
1	14.2	61.7	51 6 AX159518	AX159518 Sequence
2	13.2	57.4	30 6 AR026622	AR026622 Sequence
3	13.2	57.4	36 9 S59756	S59756 IgVHpre-B-Sequence
4	13	56.5	34 6 AX007196	AX007196 Sequence
5	13	56.5	34 6 AX007368	AX007368 Sequence
6	13	56.5	51 6 AX160002	AX160002 Sequence
7	13	56.5	52 7 PQBMS5E	PQBMS5E
8	13	56.5	52 7 PQBSS3E	PQBSS3E
9	12.8	55.7	41 6 A93667	A93667 Sequence
10	12.8	55.7	50 6 AX158612	AX158612 Sequence
11	12.8	55.7	51 6 AX159517	AX159517 Sequence
12	12.6	54.8	27 6 AR126102	AR126102 Sequence
13	12.6	54.8	27 6 AX117880	AX117880 Sequence
14	12.6	54.8	39 6 AR009156	AR009156 Sequence
15	12.6	54.8	39 6 I49577	I49577 Sequence
16	12.6	54.8	51 6 AX158897	AX158897 Sequence
17	12.6	54.8	51 6 AX158898	AX158898 Sequence
18	12.4	53.9	26 6 AX003626	AX003626 Sequence
19	12.4	53.9	33 9 HUMIGHABM	L06998 Human 1g re
20	12.4	53.9	44 10 RATMLC134	K02426 Rat fast my
21	12.4	53.9	46 6 A16157	A16157 primer 10/
22	12.4	53.9	51 6 AX116281	AX116281 Sequence
23	12.4	53.9	51 10 AF005618	AF005618 Mus muscu
24	12.4	53.9	55 9 S77443	S77443 Ig VH-immun
25	12.2	53.0	40 6 AR053641	AR053641 Sequence
26	12.2	53.0	40 6 AR033647	AR033647 Sequence
27	12.2	53.0	44 6 AX034957	AX034957 Sequence
28	12.2	53.0	45 6 AR139753	AR139753 Sequence
29	12	52.2	20 6 AR100167	AR100167 Sequence
30	12	52.2	20 6 AR137857	AR137857 Sequence
31	12	52.2	20 6 AR149851	AR149851 Sequence
32	12	52.2	20 6 I77253	I77253 Sequence
33	12	52.2	25 6 AR125844	AR125844 Sequence
34	12	52.2	26 6 AR126103	AR126103 Sequence
35	12	52.2	26 6 AR140988	AR140988 Sequence
36	12	52.2	26 6 AR125766	AR125766 Sequence
37	12	52.2	30 6 E27394	E27394 Process
38	12	52.2	30 6 E27394	E27394 Sequence
39	12	52.2	30 6 E47178	E47178 Sequence
40	12	52.2	31 6 A17338	A17338 Partial Int
41	12	52.2	35 6 AR140989	AR140989 Sequence
42	12	52.2	37 6 T3928	T3928 Sequence
43	12	52.2	39 6 E11361	E11361 DNA encodin
44	12	52.2	40 6 I86249	I86249 Sequence
45	12	52.2	45 6 A28989	A28989 oligo 8 fro

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

FEATURES
source

Location/Qualifiers
1. .36
/organism="Homo sapiens"
/db_xref="taxon:9606"
/partial
/gene="IgVH"
/note="pre-B-specific immunoglobulin heavy chain variable
a region"

Query Match 61.7%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;

BASE COUNT 13 a 16 g 5 t
ORIGIN

RESULT 2

Query Match 61.7%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;

LOCUS AR026622 30 bp DNA
DEFINITION Sequence 14 from patent US 5856121.
ACCESSION AR026622
VERSION AR026622.1 GI:5937462
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Gorski,D.H. and Walsh,K.
TITLE Growth arrest homeobox gene
JOURNAL Patent: US 5856121-A 14 JAN-1999;
FEATURES source
1..30
/organism="unknown"
BASE COUNT 4 a 13 c 8 g 5 t
ORIGIN

RESULT 4

Query Match 57.4%; Score 13.2; DB 6; Length 36;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;

LOCUS AX007196 34 bp DNA
DEFINITION Sequence 36 from Patent WO0000618.
ACCESSION AX007196
VERSION AX007196.1 GI:9995062
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 34)
AUTHORS Leadlay,P.F., Cortes,J., Staunton,J. and McArthur,H.A.
TITLE Polypeptides and their synthesis
JOURNAL Patent: WO 0000618-A 36 JAN-2000;
LEADLAY PETER FRANCIS (GB); CORTES JESUS (GB); STAUNTON JAMES (GB);
BIOTICA TECH LTD (GB); MCARTHUR HAMISH ALASTAIR IRVIN (US)
FEATURES source
1..34
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 7 a 10 c 8 g 9 t
ORIGIN

RESULT 3

Query Match 55.5%; Score 13; DB 6; Length 34;
Best Local Similarity 76.2%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 5;
Indels 0; Gaps 0;

LOCUS S59766 36 bp mRNA
DEFINITION PR1 20-MAR-2000
IGH-pre-B-specific immunoglobulin heavy chain variable region
(CDR3 region, V-D-J rearrangement, clone LE 1-17) [human, bone
marrow, mRNA Recombinant Partial, 36 nt].
ACCESSION S59766
VERSION S59766.1 GI:385405
KEYWORDS

SOURCE Human bone marrow.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS Milii,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
Fougereff,M. and Schiff,C.
TITLE Bone marrow cells in X-linked agammaglobulinemia express
pre-B-specific genes (lambda-like and V preB) and present
immunoglobulin V-D-J gene usage strongly biased to a fetal-like
repertoire
J. Clin. Invest. 91 (4), 1616-1629 (1993)
JOURNAL MEDLINE
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 131828] from the original Journal article.
This sequence comes from Fig. 3.
Map location: X.

FEATURES
source

Location/Qualifiers
1. .36
/organism="Homo sapiens"
/db_xref="taxon:9606"
/partial
/gene="IgVH"
/note="pre-B-specific immunoglobulin heavy chain variable
a region"

Query Match 57.4%; Score 13.2; DB 9; Length 36;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;

BASE COUNT 6 a 3 c 15 g 12 t
ORIGIN

RESULT 5

Query Match 55.5%; Score 13; DB 6; Length 34;
Best Local Similarity 76.2%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 5;
Indels 0; Gaps 0;

LOCUS AX007368 34 bp DNA
DEFINITION Sequence 36 from Patent WO0000500.
ACCESSION AX007368
VERSION AX007368.1 GI:9995138
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 34)
AUTHORS Leadlay,P.F., Cortes,J., Staunton,J. and McArthur,H.A.
TITLE Polyketides and their synthesis
JOURNAL Patent: WO 0000500-A 36 JAN-2000;
LEADLAY PETER FRANCIS (GB); CORTES JESUS (GB); STAUNTON JAMES (GB);
BIOTICA TECH LTD (GB); PFIZER (US); MCARTHUR HAMISH ALASTAIR IRVIN
(US)

FEATURES		source		Location/Qualifiers	
source	1. .34	/organism="synthetic construct"		1. .52	/organism="Bacteriophage Q-beta"
ORGIN		/db_xref="taxon:32630"		15 a	/db_xref="taxon:12009" 9 t
BASE COUNT	7 a	10 c	8 g	11 c	17 g
RESULT	6	Query Match	56.5%	Score 13; DB 6;	Length 34;
LOCUS	AX160002	Best Local Similarity	76.2%	Pred. No. 2.9e+04;	
DEFINITION	Sequence 3330 from Patent WO0140521.	Matches	16;	Conservative	0;
ACCESSION	AX160002	Mismatches	5;	Indels	0;
VERSION	AX160002.1	Gaps	0;		
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
REFERENCE	1 (bases 1 to 51)				
AUTHORS	Shinkles, R.A. and Leach, M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 010521-A 3330 07-JUN-2001;				
CURAGEN	Corporation (US)				
FEATURES	Location/Qualifiers				
source	1. .51				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
misc_feature	26	/note="2 of 2 allelic variants (3329 is other entry)			
BASE COUNT	15 a	Accession number cg43247175	13 c	14 g	9 t
ORIGIN					
RESULT	7	Query Match	56.5%	Score 13; DB 6;	Length 51;
POBMS5E	POBMS5E	Best Local Similarity	76.2%	Pred. No. 2.9e+04;	
LOCUS	52 bp	Matches	16;	Conservative	0;
DEFINITION	mRNA	Mismatches	5;	Indels	0;
ACCESSION	PHG	Gaps	0;		
VERSION	M57754				
KEYWORDS					
SOURCE	Bacteriophage Q-beta RNA.				
ORGANISM	Bacteriophage Q-beta				
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Leviviridae;					
Alloleviviruses; Allolevivivirus subgroup III.					
Allolevivirus; Allolevivirus subgroup III.					
REFERENCE	1 (bases 1 to 52)				
AUTHORS	Goodman, H.M., Billeter, M.A., Hindley, J. and Weissmann, C.				
TITLE	The nucleotide sequence at the 5'-terminus of the Q-beta RNA minus strand				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 67, 921-928 (1970)				
FEATURES	Location/Qualifiers				
source	1. .52				
	/organism="Bacteriophage Q-beta"				
	/db_xref="taxon:12009"				
BASE COUNT	9 a	17 c	11 g	15 t	
ORIGIN					
RESULT	9	Query Match	56.5%	Score 13; DB 7;	Length 52;
POBMS5E	POBMS5E	Best Local Similarity	76.2%	Pred. No. 2.9e+04;	
LOCUS	52 bp	Matches	16;	Conservative	0;
DEFINITION	mRNA	Mismatches	5;	Indels	0;
ACCESSION	PHG	Gaps	0;		
VERSION	M57754.1				
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
REFERENCE	artificial sequence.				
AUTHORS	1 (bases 1 to 41)				
TITLE	Langer, G. and Toschi, L.				
JOURNAL	METHOD OF DEFECTING THE EFFECT OF TEST SUBSTANCES USING HEN UROKINASE				
FEATURES	Patent: WO 9734144-A 3 18-SEP-1997;				
source	SCHERING AG (DE); LANGER GERNOT (DE)				
BASE COUNT	5 a	14 c	15 g	7 t	
ORIGIN					
COMMENT	/organism="synthetic construct"				
JOURNAL	/db_xref="taxon:32630"				
FEATURES	From EMBL 27 entry POBMS5E; dated 13-FEB-1991.				
COMMENT	Location/Qualifiers				

ORIGIN							
Query Match	55.7%	Score 12.8;	DB 6;	Length 41;			
Best Local Similarity	87.5%	Pred. No. 3.7e-04;					
Matches	14;	Conservative	0;	Mismatches	2;	Indels	0;
Qy	4 aaccggcgatctccg	19				Gaps	0;
Db	33 ACCACCGGTTCTCG	18					
RESULT	10						
AX158612/c	AX158612	50 bp	DNA		PAT	22-JUN-2001	
LOCUS							
DEFINITION	Sequence 1940 from Patent WO0140521.						
ACCESSION	AX158612						
VERSION	AX158612.1						
KEYWORDS	human.						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 50)						
AUTHORS	Shimkets,R.A. and Leach,M.						
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof						
JOURNAL	Patent: WO 0140521-A 1940 07-JUN-2001; Curagen Corporation (US)						
FEATURES	Location/Qualifiers						
source	1..50						
misc_feature	/note="organism="Homo sapiens"						
	/db_xref="taxon:9606"						
misc_feature	/note="2 of 2 allelic variants (1939 is other entry)"						
BASE COUNT	11 a	13 c	18 g	8 t			
ORIGIN							
Query Match	55.7%	Score 12.8;	DB 6;	Length 50;			
Best Local Similarity	87.5%	Pred. No. 3.8e+04;					
Matches	14;	Conservative	0;	Mismatches	2;	Indels	0;
Qy	1 gagaacacccgttc	16				Gaps	0;
Db	28 GAGTACGCCGCCTC	13					
RESULT	11						
AX15517	AX15517	51 bp	DNA		PAT	22-JUN-2001	
LOCUS							
DEFINITION	Sequence 2845 from Patent WO0140521.						
ACCESSION	AX15517						
VERSION	AX15517.1						
KEYWORDS	human.						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 51)						
AUTHORS	Shimkets,R.A. and Leach,M.						
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof						
JOURNAL	Patent: WO 0140521-A 2845 07-JUN-2001; Curagen Corporation (US)						
FEATURES	Location/Qualifiers						
source	1..51						
	/note="organism="Homo sapiens"						
misc_feature	/db_xref="taxon:9606"						
	/note="1 of 2 allelic variants (2846 is other entry)"						
BASE COUNT	13 a	16 c	17 g	5 t			
ORIGIN							
Query Match	55.7%	Score 12.8;	DB 6;	Length 51;			
Best Local Similarity	87.5%	Pred. No. 3.8e+04;					
Matches	14;	Conservative	0;	Mismatches	2;	Indels	0;
Qy	3 gaacacccgttc	18				Gaps	0;
Db	9 GAACCCAGTCCTC	24					
RESULT	12						
AR126102/c	AR126102	27 bp	DNA		PAT	16-MAY-2001	
LOCUS							
DEFINITION	Sequence 444 from patent US 6177557.						
ACCESSION	AR126102						
VERSION	AR126102.1						
KEYWORDS	.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 27)						
AUTHORS	JanJic,N., Gold,L. and Tasset,D.						
TITLE	High affinity ligands of basic fibroblast growth factor and thrombin						
JOURNAL	Patent: US 6177557-A 444 23-JAN-2001;						
FEATURES	Location/Qualifiers						
source	1..27						
BASE COUNT	4 a	3 c	13 g	6 t		1 others	
ORIGIN							
Query Match	54.8%	Score 12.6;	DB 6;	Length 27;			
Best Local Similarity	75.0%	Pred. No. 4.6e+04;					
Matches	15;	Conservative	0;	Mismatches	5;	Indels	0;
Qy	1 gagaacacccgttcgtcgcaa	23				Gaps	0;
Db	27 GHACACCCGCGCTTCACA	5					
RESULT	13						
AX117880/c	AX117880	27 bp	DNA		PAT	11-MAY-2001	
LOCUS							
DEFINITION	Sequence 3003 from Patent WO0129262.						
ACCESSION	AX117880						
VERSION	AX117880.1						
KEYWORDS	.						
SOURCE	synthetic construct.						
ORGANISM	synthetic construct.						
REFERENCE	1 (bases 1 to 27)						
AUTHORS	Picoult-Newburg,L. and Pohl,M.						
TITLE	Genotyping reagents, kits and methods of use thereof						
JOURNAL	Patent: WO 0128262-A 303 26-APR-2001; Orchid Biosciences, Inc. (US)						
FEATURES	Location/Qualifiers						
source	1..27						
	/note="organism="synthetic construct"						
	/db_xref="taxon:32650"						
	/note="Primer"						
BASE COUNT	4 a	5 c	11 g	6 t		1 others	
ORIGIN							
Query Match	54.8%	Score 12.6;	DB 6;	Length 27;			
Best Local Similarity	75.0%	Pred. No. 4.6e+04;					
Matches	15;	Conservative	0;	Mismatches	5;	Indels	0;
Qy	3 gaacacccgttc	18				Gaps	0;
Db	9 GAACCCAGTCCTC	24					

Qy	2	aggaaacccgttcctcgca	21
Db	23	ACANAAACCGCCATGCGCA	4
RESULT	14		
AR069156			
LOCUS	AR069156	39 bp	DNA
DEFINITION	Sequence 26 from patent US 5891442.		PAT
ACCESSION	AR069156		
VERSION	AR069156.1	GI:7220044	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 39)		
AUTHORS	Paoletti,E., Taylor,J. and Getting,R.		
TITLE	Infectious bursal disease virus recombinant poxvirus vaccine		
JOURNAL	Patent: US 5891442-A 26 06 APR-1999;		
FEATURES	Location/Qualifiers		
SOURCE	1. 39 /organism="unknown"		
BASE COUNT	10 a 12 c 10 g	7 t	
ORIGIN			
RESULT	15		
149577			
LOCUS	149577	39 bp	DNA
DEFINITION	Sequence 26 from patent US 5891442.		PAT
ACCESSION	149577		
VERSION	149577.1	GI:2471797	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 39)		
AUTHORS	Paoletti,E., Taylor,J. and Getting,R.		
TITLE	Infectious bursal disease virus recombinant poxvirus vaccine		
JOURNAL	Patent: US 5891442-A 26 06 APR-1999;		
FEATURES	Location/Qualifiers		
SOURCE	1. 39 /organism="unknown"		
BASE COUNT	10 a 12 c 10 g	7 t	
ORIGIN			
Query Match	54.8%	Score 12.6; DB 6;	Length 39;
Best Local Similarity	78.9%	Pred. No. 4.7e+04;	
Matches	15;	Mismatches 4;	
Indels	0;	Gaps	
Qy	4	aacacccgcctctgcaa	22
Db	3	AACACGAGCTCTCCCCAA	21

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